RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: <u>09/301,380A</u>
Source: <u>1FW16,</u>
Date Processed by STIC: <u>6/2/06</u>

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _09/301,380A_   CRF Edit Date: _6/2/06_
                                       Edited by: _AZ_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

____ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

_✓_ Other: _deleted number under stop codon - Sequence 1_
Sequence 2 - corrected amino acid numbering
_____

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                RAW SEQUENCE LISTING              DATE: 06/02/2006
                PATENT APPLICATION:  US/09/301,380A   TIME: 09:38:41

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                Output Set: N:\CRF4\06022006\I301380A.raw

  3 <110> APPLICANT: Murphy, Gerald P.
  4        Boynton, Alton L.
  5        Sehgal, Anil
  7 <120> TITLE OF INVENTION: Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS
  8        FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS
 10 <130> FILE REFERENCE: 20093A-002100US
 12 <140> CURRENT APPLICATION NUMBER: 09/301,380A
C--> 13 <141> CURRENT FILING DATE: 2001-06-15
 15 <150> PRIOR APPLICATION NUMBER: 60/112,098
 16 <151> PRIOR FILING DATE: 1998-12-14
 18 <150> PRIOR APPLICATION NUMBER: 60/083,152
 19 <151> PRIOR FILING DATE: 1998-04-27
 21 <160> NUMBER OF SEQ ID NOS: 33
 23 <170> SOFTWARE: PatentIn Ver. 2.0
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 41            1               5                  10
 43 att ctc ttc ctg tgc cag atg att agt gca ctg gaa gta cct ctt gat    219
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 45  15              20               25                  30
 47 cca aaa ctt ctt gaa gac ttg gta cag cct cca acc atc acc caa cag    267
 48 Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln
 49              35               40                  45
 51 tct cca aaa gat tac att att gac cct cgg gag aat att gta atc cag    315
 52 Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln
 53           50               55                  60
 55 tgt gaa gcc aaa ggg aaa ccg ccc cca agc ttt tcc tgg acc cgt aat    363
 56 Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn
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 60 Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro
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 63 ggc aca gga acg ctc ata att aac atc atg agc gaa ggg aaa gct gag    459
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68 Thr Tyr Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu Arg Gly Ala
69                    115                120                125
71 gca gtt tct aat aac att gtt gtc cgc cca tcc aga tca cca ttg tgg    555
72 Ala Val Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser Pro Leu Trp
73             130                135                140
75 acc aaa gaa aaa ctt gaa cca atc aca ctt caa agt ggt cag tct tta    603
76 Thr Lys Glu Lys Leu Glu Pro Ile Thr Leu Gln Ser Gly Gln Ser Leu
77         145                150                155
79 gta ctt ccc tgc aga ccc cca att gga tta cca cca cct ata ata ttt    651
80 Val Leu Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro Ile Ile Phe
81     160                165                170
83 tgg atg gat aat tcc ttt caa aga ctt cca caa agt gag aga gtt tct    699
84 Trp Met Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu Arg Val Ser
85 175                180                185                190
87 caa ggt ttg aat ggg gac ctt tat ttt tcc aat gtc ctc cca gag gac    747
88 Gln Gly Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu Pro Glu Asp
89                    195                200                205
91 acc cgc gaa gac tat atc tgt tat gct aga ttt aat cat act caa acc    795
92 Thr Arg Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His Thr Gln Thr
93         210                215                220
95 ata cag cag aag caa cct att tct gtg aag gtg att tca gtg gat gaa    843
96 Ile Gln Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser Val Asp Glu
97         225                230                235
99 ttg aat gac act ata gct gct aat ttg agt gac act gag ttt tat ggt    891
100 Leu Asn Asp Thr Ile Ala Ala Asn Leu Ser Asp Thr Glu Phe Tyr Gly
101     240                245                250
103 gct aaa tca agt aga gag agg cca cca aca ttt tta act cca gaa ggc    939
104 Ala Lys Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly
105 255                260                265                270
107 aat gca agt aac aaa gag gaa tta aga gga aat gtg ctt tca ctg gag    987
108 Asn Ala Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu
109                    275                280                285
111 tgc att gca gaa gga ctg cct acc cca att att tac tgg gca aag gaa   1035
112 Cys Ile Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu
113         290                295                300
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116 Asp Gly Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys
117         305                310                315
119 acc ttg cag atc att cat gtt tca gaa gca gac tct gga aat tac caa   1131
120 Thr Leu Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly Asn Tyr Gln
121     320                325                330
123 tgt ata gca aaa aat gca tta gga gcc atc cac cat acc att tct gtt   1179
124 Cys Ile Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val
125 335                340                345                350
127 aga gtt aaa gcg gct cca tac tgg atc aca gcc cct caa aat ctt gtg   1227
128 Arg Val Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val
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133                   370                   375                   380
135 ccc aaa ccc aga att agc tgg tta aca aat gga gtc cca ata gaa att   1323
136 Pro Lys Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile
137                   385                   390                   395
139 gcc cct gat gac ccc agc aga aaa ata gat ggc gat acc att att ttt   1371
140 Ala Pro Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr Ile Ile Phe
141         400                   405                   410
143 tca aat gtt caa gaa aga tca agt gca gta tat cag tgc aat gcc tct   1419
144 Ser Asn Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser
145 415                   420                   425                   430
147 aat gaa tat gga tat tta ctg gca aac gca ttt gta aat gtg ctg gct   1467
148 Asn Glu Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala
149                   435                   440                   445
151 gag cca cca cga atc ctc aca cct gca aac aca ctc tac cag gtc att   1515
152 Glu Pro Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile
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155 gca aac agg cct gct tta cta gac tgt gcc ttc ttt ggg tct cct ctc   1563
156 Ala Asn Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu
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159 cca acc atc gag tgg ttt aaa gga gct aaa gga agt gct ctt cat gaa   1611
160 Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu
161         480                   485                   490
163 gat att tat gtt tta cat gaa aat gga act ttg gaa atc aaa gat gct   1659
164 Asp Ile Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala
165 495                   500                   505                   510
167 aca tgg atc gtt aaa gaa att cct gtg gcc caa aag gac agt aca gga   1707
168 Thr Trp Ile Val Lys Glu Ile Pro Val Ala Gln Lys Asp Ser Thr Gly
169                   515                   520                   525
171 act tat acg tgt gtt gca agg aat aaa tta ggg atg gca aag aat gaa   1755
172 Thr Tyr Thr Cys Val Ala Arg Asn Lys Leu Gly Met Ala Lys Asn Glu
173                   530                   535                   540
175 gtt cac tta cag ccc gaa tat gca gtt gtg caa aga ggg agc atg gtg   1803
176 Val His Leu Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val
177         545                   550                   555
179 tcc ttt gaa tgc aaa gtg aaa cat gat cac acc tta tcc ctc act gtc   1851
180 Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val
181         560                   565                   570
183 ctg tgg ctg aag gac aac agg gaa ctg ccc agt gat gaa agg ttc act   1899
184 Leu Trp Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr
185 575                   580                   585                   590
187 gtt gac aag gat cat cta gtg gta gct gat gtc agt gac gat gac agc   1947
188 Val Asp Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser
189                   595                   600                   605
191 ggg acc tac acg tgt gtg gcc aac acc act ctg gac agc gtc tcc gcc   1995
192 Gly Thr Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala
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200 Tyr Asp Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu
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203 gac aaa agt gtt cag ctg tca tgg acc cca ggc gat gac aac aat agc   2139
204 Asp Lys Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser
205 655                 660                 665                 670
207 ccc att aca aaa ttc atc atc gaa tat gaa gat gca atg cac aag cca   2187
208 Pro Ile Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro
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212 Gly Leu Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala
213             690                 695                 700
215 cag ctg aag ctg tct cct tac gtg aac tac tcc ttc cgc gtg atg gca   2283
216 Gln Leu Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala
217         705                 710                 715
219 gtg aac agc att ggg aag agc ttg ccc agc gag gcg tct gag cag tat   2331
220 Val Asn Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr
221         720                 725                 730
223 ttg acg aaa gcc tca gaa cca gat aaa aac ccc aca gct gtg gaa gga   2379
224 Leu Thr Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly
225 735                 740                 745                 750
227 ctg gga tca gag cct gat aat ttg gag att acg tgg aag ccc ttg aat   2427
228 Leu Gly Ser Glu Pro Asp Asn Leu Glu Ile Thr Trp Lys Pro Leu Asn
229             755                 760                 765
231 ggt ttc gaa tct aat ggg cca ggc ctt cag tac aaa gtt agc tgg cgc   2475
232 Gly Phe Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg
233             770                 775                 780
235 cag aaa gat ggt gat gat gaa tgg aca tct gtg gtt gtg gca aat gta   2523
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237         785                 790                 795
239 tcc aaa tat att gtc tca ggc acg cca acc ttt gtt cca tac ctg atc   2571
240 Ser Lys Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile
241         800                 805                 810
243 aaa gtt cag gcc ctg aat gac atg ggg ttt gcc ccc gag cca gct gta   2619
244 Lys Val Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val
245 815                 820                 825                 830
247 gtc atg gga cat tct gga gaa gac ctc cca atg gtg gct cct ggg aac   2667
248 Val Met Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn
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255 cca gta cct ctg aaa agc atc cga gga cac cta caa ggc tat cgg att   2763
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264 Glu Lys Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu
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267 ccg ggg cta gag ccc ttt agc cac tac aca ctg aat gtc cga gtg gtc   2907
268 Pro Gly Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val
269                 915                 920                 925
271 aat ggg aaa ggg gag ggc cca gcc agc cct gac aga gtc ttt aat act   2955
272 Asn Gly Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr
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275 cca gaa gga gtc ccc agt gct ccc tcg tct ttg aag att gtg aat cca   3003
276 Pro Glu Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro
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279 aca ctg gac tct ctc act ttg gaa tgg gat cca ccg agc cac ccg aat   3051
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315 gaa tgg aga aaa gaa att gta aat ggt tct cgg agc ttc ttt ggg tta   3483
316 Glu Trp Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu
317         1105                1110                1115
319 aag ggt cta atg cca gga aca gca tac aaa gtt cga gtt ggt gct gtg   3531
320 Lys Gly Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/02/2006
PATENT APPLICATION: US/09/301,380A   TIME: 09:38:42

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF4\06022006\I301380A.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 1

VERIFICATION SUMMARY　　　　　　　　DATE: 06/02/2006
PATENT APPLICATION:　**US/09/301,380A**　　TIME: 09:38:42

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF4\06022006\I301380A.raw**

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0

Raw Sequence Listing before editing (for reference only)

RAW SEQUENCE LISTING   DATE: 06/01/2006
PATENT APPLICATION: US/09/301,380A   TIME: 12:11:12

Input Set : A:\20093A-21US-Substitute Sequence Listing.txt
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   3 <110> APPLICANT: Murphy, Gerald P.
   4        Boynton, Alton L.
   5        Sehgal, Anil
   7 <120> TITLE OF INVENTION: Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS
   8        FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS
  10 <130> FILE REFERENCE: 20093A-002100US
  12 <140> CURRENT APPLICATION NUMBER: 09/301,380A
C--> 13 <141> CURRENT FILING DATE: 2001-06-15
  15 <150> PRIOR APPLICATION NUMBER: 60/112,098
  16 <151> PRIOR FILING DATE: 1998-12-14
  18 <150> PRIOR APPLICATION NUMBER: 60/083,152
  19 <151> PRIOR FILING DATE: 1998-04-27
  21 <160> NUMBER OF SEQ ID NOS: 33
  23 <170> SOFTWARE: PatentIn Ver. 2.0
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ERRORED SEQUENCES

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 372 <210> SEQ ID NO: 2
 373 <211> LENGTH: 1299
 374 <212> TYPE: PRT
 375 <213> ORGANISM: Homo sapiens
 377 <400> SEQUENCE: 2
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 382                  20                  25                  30
 384 Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln Ser Pro
 385              35                  40                  45
 387 Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln Cys Glu
 388          50                  55                  60
 390 Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn Gly Thr
 391  65                  70                  75                  80
 393 His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro Gly Thr
 394                  85                  90                  95
 396 Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly Lys Ala Glu Thr Tyr
 397              100                 105                 110
 399 Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu Arg Gly Ala Ala Val
 400          115                 120                 125
 402 Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser Pro Leu Trp Thr Lys
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 406 145                 150                 155                 160
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415         195             200             205
417 Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His Thr Gln Thr Ile Gln
418     210             215                 220
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421 225             230             235             240
423 Asp Thr Ile Ala Ala Asn Leu Ser Asp Thr Glu Phe Tyr Gly Ala Lys
424             245             250             255
426 Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly Asn Ala
427         260             265             270
429 Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu Cys Ile
430         275             280             285
432 Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu Asp Gly
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436 305             310             315             320
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466 465             470             475             480
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469             485             490             495
471 Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala Thr Trp
472         500             505             510
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489 Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser Gly Thr
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493       610                    615                    620
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496 625                    630                    635                    640
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502                    660                    665                    670
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505            675                    680                    685
507 Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala Gln Leu
508       690                    695                    700
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511 705                    710                    715                    720
513 Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr Leu Thr
514                    725                    730                    735
516 Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly Leu Gly
517                    740                    745                    750
519 Ser Glu Pro Asp Asn Leu Glu Ile Thr Trp Lys Pro Leu Asn Gly Phe
520            755                    760                    765
522 Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg Gln Lys
523       770                    775                    780
525 Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val Ser Lys
526 785                    790                    795                    800
528 Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile Lys Val
529                    805                    810                    815
531 Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val Val Met
532            820                    825                    830
534 Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn Val Arg
535            835                    840                    845
537 Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp Pro Val
538       850                    855                    860
540 Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile Tyr Tyr
541 865                    870                    875                    880
543 Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile Glu Lys
544                    885                    890                    895
546 Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu Pro Gly
547            900                    905                    910
549 Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val Asn Gly
550            915                    920                    925
552 Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr Pro Glu
553       930                    935                    940
```

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555 Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro Thr Leu
556 945                 950                 955                 960
558 Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn Gly Ile
559                 965                 970                 975
561 Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr His Glu
562                 980                 985                 990
564 Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr Arg Trp
565             995             1000                1005
567 Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr Phe Tyr
568    1010                1015                1020
570 Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu Ala Val
571 025 /025             1030                1035                1040
573 Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly Ala Gly
574                1045                1050                1055
576 Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala Ala Ala
577             1060                1065                1070
579 Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro Glu His
580          1075                1080                1085
582 Val Asn Phe Tyr Val Gln Tyr Gly Val Ala Gly Ser Lys Glu Glu Trp
583    1090                1095                1100
585 Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu Lys Gly
586 105 /105             1110                1115                1120
588 Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val Gly Asp
589             1125                1130                1135
591 Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro Ala Met
592             1140                1145                1150
594 Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile Gly Leu
595          1155                1160                1165
597 Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Leu Ile Val Cys Phe
598    1170                1175                1180
600 Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys Glu Asp
601 185 /185             1190                1195                1200
603 Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp Asp Gly Thr
604                1205                1210                1215
606 Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys Lys Gly
607          1220                1225                1230
609 Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser Asp Asp
610    1235                1240                1245
612 Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly Gln Phe Asn Glu Asp
613    1250                1255                1260
615 Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu Pro Ala
616 265 /265             1270                1275                1280
618 Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro Val Asn Ala Met Asn
619             1285                1290                1295
621 Ser Phe Val
```

E--> 571
E--> 586
E--> 601
E--> 616

VERIFICATION SUMMARY   DATE: 06/01/2006
PATENT APPLICATION: **US/09/301,380A**   TIME: 12:11:14

Input Set : **A:\20093A-21US-Substitute Sequence Listing.txt**
Output Set: **N:\CRF4\06012006\I301380A.raw**

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:365 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:571 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:586 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:601 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:616 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
I:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0